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INFORMATION DISCLOSURE STATEMENT BY APPLICANT <i>(Use as many sheets as necessary)</i>				Application Number	10/722,033
Sheet	1	Of	2	Filing Date	November 25, 2003
				First Named Inventor	Satoru Miyano
				Art Unit	1631
				Examiner Name	Pablo S. Whaley
				Attorney Docket Number	34569-701.201

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/PW/	1.	AKAIKE, H. A new look at the statistical model identification. (Originally published in IEEE Trans. Automat. Contr. 1974; 19:716-723.)	
	2.	AKAIKE, H. Information theory and an extension of the maximum likelihood principle. (Originally published in B.N. Petrov and F. Csaki (editors), 2nd Int. Symp. on Inf. Theory. Akadémiai Kiadó, Budapest. 1973; 267-281.)	
	3.	ANDERSON, et al. eds. The New Statistical Analysis of Data. Springer Verlag, New York. 1996. (Table of Contents only.)	
	4.	DERISI, et al. Exploring the metabolic and genetic control of gene expression on a genomic scale. Science. 1997; 278(24):680-686.	
	5.	EISEN, et al. Cluster analysis and display of genome-wide expression patterns. Proc. Natl. Acad. Sci. USA. 1998; 95:14863-14868.	
	6.	FRIEDMAN, et al. Using Bayesian networks to analyze expression data. J. Comp. Biol. 2000; 7:601-620.	
	7.	HIHARA, et al. DNA microarray analysis of cyanobacterial gene expression during acclimation to high light. The Plant Cell. 2001; 13:793-806.	
	8.	HOON, et al. Statistical analysis of a small set of time-ordered gene expression data using linear splines. Bioinformatics. 2002; 18:1477-1485.	
	9.	HORN, et al. Eds. Matrix Analysis. Cambridge University Press, Cambridge, UK. 1999. (Table of Contents only)	
↓	10.	IMOTO, et al. Bayesian network and nonparametric heteroscedastic regression for nonlinear modeling of genetic network. Proc. IEEE Computer Society Bioinformatics Conference. 2002; 219-227.	

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/PW/	11.	IMOTO, et al. Estimation of genetic networks and functional structures between genes by using Bayesian networks and nonparametric regression. <i>Pac. Symp. on Biocomputing</i> . 2002; 7:175-186.		T ⁶
	12.	LIANG, et al. REVEAL, a general reverse engineering algorithm for inference of genetic network architectures. <i>Pac. Symp. on Biocomputing</i> . 1998; 3:18-29.		
	13.	MATSUNO, et al. XML documentation of biopathways and their simulation in Genomic Object Net. <i>Genome Informatics</i> . 2001; 12:54-62.		
	14.	MOSZER, et al. SubtiList: the reference database for the <i>Bacillus subtilis</i> genome. <i>Nucleic Acids Research</i> . 2002; 30(1):62-65.		
	15.	MOSZER, I. The complete genome of <i>Bacillus subtilis</i> : From sequence annotation to data management and analysis. <i>FEBS Letters</i> . 1998; 430:28-36.		
	16.	PRIESTLEY, M. B. <i>Spectral Analysis and Time Series</i> . Academic Press, London. 1994. (Table of Contents only.)		
	17.	SAKAMOTO, et al. Evolutionary inference of a biological network as differential equations by genetic programming. <i>Genome Informatics</i> . 2001; 12:276-277.		
	18.	SPELLMAN, et al. Comprehensive identification of cell cycle-regulated genes of the yeast <i>Saccharomyces cerevisiae</i> by microarray hybridization. <i>Mol. Biol. Cell</i> . 1998; 9:3273-3297.		
▼	19.	TAMAYO, et al. Interpreting patterns of gene expression with self-organizing maps: Methods and application to hematopoietic differentiation. <i>Proc. Natl. Acad. Sci. USA</i> . 1999; 96:2907-02912.		

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